

1 TCGGTCGCCTGAGAGGTATCACCTCTCTTGGGCTCAAGATGGACAAAGAGCGCCTGGCCTACGCCATCATCCAGTTCCTGTCATGACACGCTCCGGCA
M D N K K R L A Y A I I Q F L H D Q L R H>

101 CGGGGCGCTCTCGTCGGATGCTCAGGAGAGCTTGGAAATGCGCATCCAGTGCCTGGAGACTGCGTTCGGGTGACGGTAGAAGACAGTACCTTCGCGCT
G G L S S D A O E S L E V A I O C L E T A F G V T V E D S D L A L >

201 CCTCAGACTCTGCCGGAGATATTTGAAGCGCTGCCACGGGCAAGGAGATGCCGCGAGGACCTGAGGAGCCCGGCGGAGCCCGCTTCGAGGAGGACT
P Q T L P E I F E A A T G K E M P Q D L R S P A R T P P S E E D S>

301 CAGCAGAGGCAGAGCGCTCAAAACCGAAGGAAACGAGCAGATGAAAGTGGAAAACCTTTGAAGCTCCGTGCTATTTCTACGGAAAAGCCATCGAGCTCAA
A E A E R L K T E G N E Q M K V E N F E A A V H F Y G K A I E L N>

401 CCCAGCCAAAGCGCTCTATTTCTCAACAGAGCGCGAGCCTACAGCAAACCTCGGCAACTACGAGCGCGGTGCGAGGACTGTGAGCGGGCCATCTGCATT
P A N A V Y F C N R A A A Y S K L G N Y A G A V O D C E R A I C I >

501 GACCGGCGCTACAGCAAGCCTACGGCAGGATGGCGCTTGGCGCTCTCCAGCCTCAACAGCACGCTGGAGCGCGCTTACTACAAGAAGCGCTGGAGC
D P A Y S K A Y G R M G L A L S S L N K H V E A V A Y Y K K A L E L>

601 TGGACCCCGACACGAGACATACAAGTCCAACCTCAAGATAGCGAGCTGAAGCTCGGGAGGCCCCAGCCCCCGGAGCGGTGGCGAGCTTCGACAT
D P D N E T Y K S N L K I A E L K L R E A P S P T G G V G S F D I>

701 CGCGGCGCTGCTGAACAACCCCTGGCTTCATGAGCATGGCTTCGAACCTAATGAACAATCCCAAGATTACAGCAGCTCATGTCCGGCATGATTTCCGGTGGC
A G L L N N P G F M S M A S N L M N N P Q I Q Q L M S G M I S G G >

801 AACAAACCCCTTGGGAACTCCCGGCACCGCCCTCGCAGAACGACCTTGGCCAGCCTCATCCAGCGGGGCCAGAGTTTCCCCAGCAGATGACGACGACGAGA
N N P L G T P G T S P S Q N D L A S L I Q A G Q Q F A Q Q M Q Q Q Q N>

FIG. 1A

2

FIG. 1B

FIG. 2A

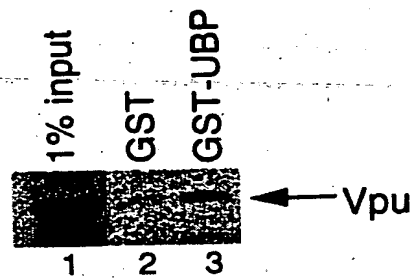


FIG. 2B

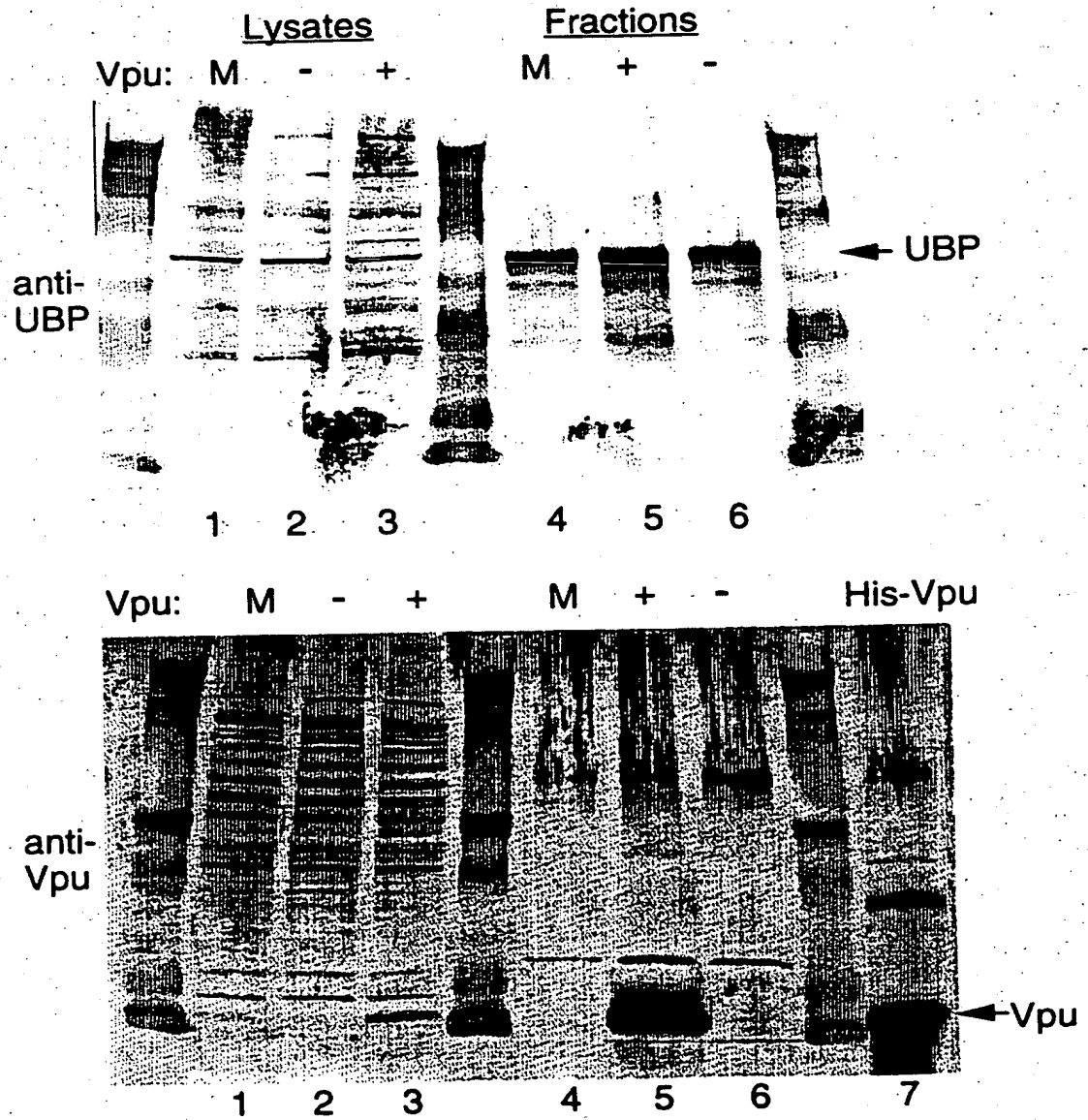


FIG 3A

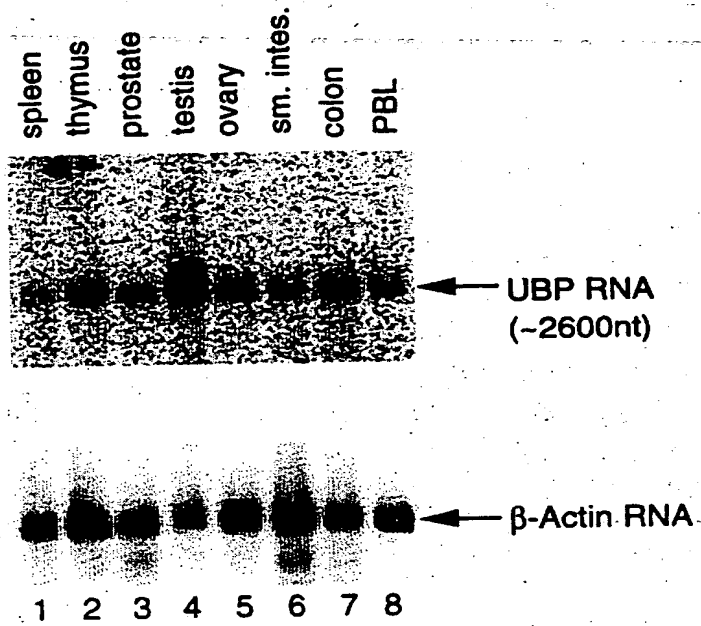


FIG 3B

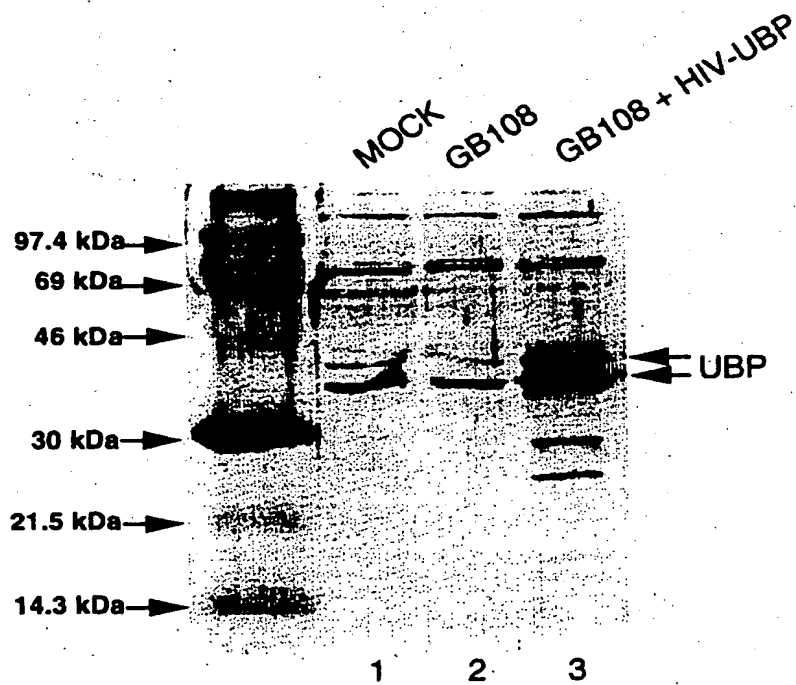
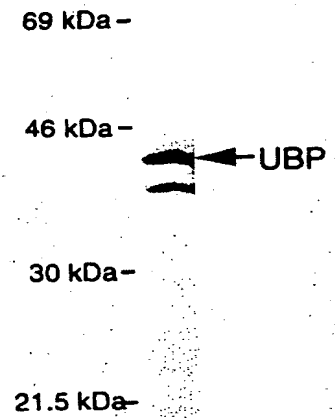


FIG 3C

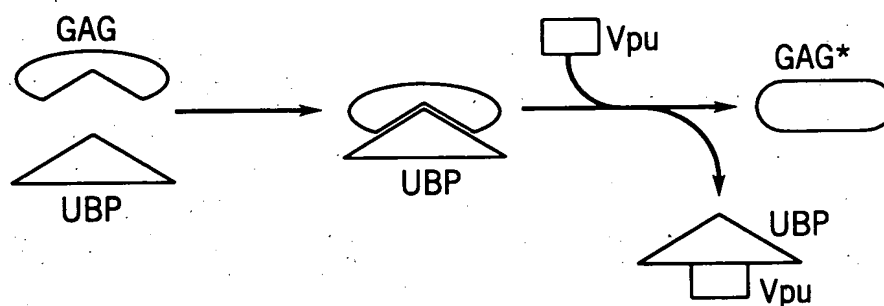
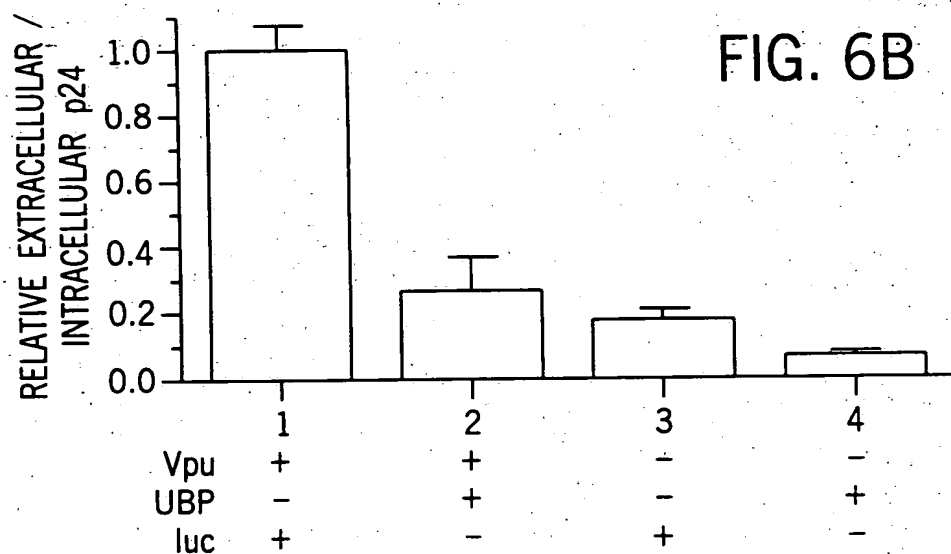
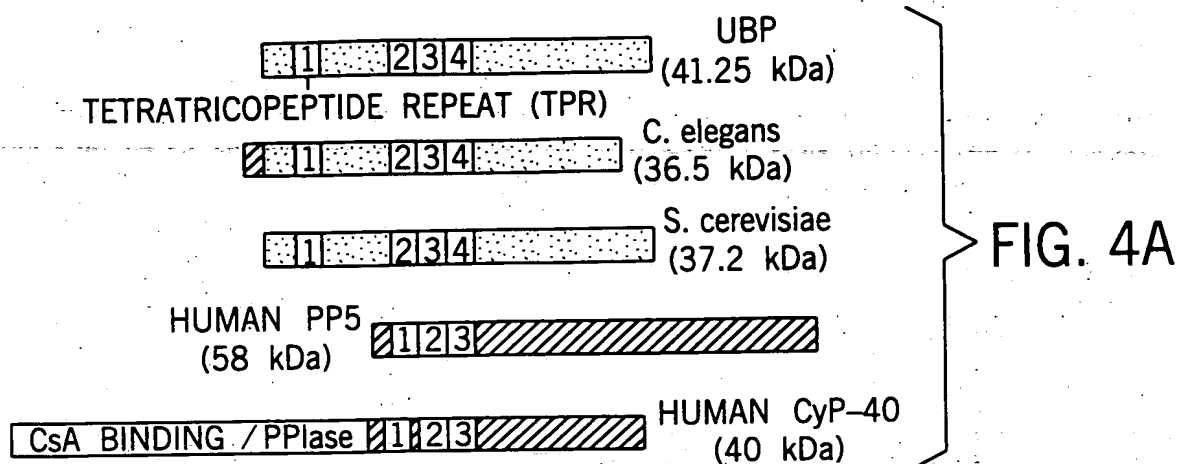


FIG. 4B

CONSENSUS * - - * G - * Y - - - - * - - - A * - - F - - A * - - * - - P - - - - - Y

UBP L R H G G L S S D A Q E S L E V A I Q C L E T A F G V T V E D S D L TPR1 (19-52)
C. eleg. V S Q N Q A T A E Q A E A L E V A I Q C L E H S F G L D D A S Y A F TPR1 (38-71)
S. cerev. V E K K E T S E D G A D S L N V A M D C I S E A F G F E R E A V S G TPR1 (20-53)

UBP L K T E G N E Q M K V E N F E A A V H F Y G K A I E L N P A N A V Y TPR2 (94-127)
C. eleg. L K E E G N D L M K A S Q F E A A V Q K Y N A A I K L N R D P V Y TPR2 (108-140)
S. cerev. L K M Q G N K A M A N K D Y E L A I N K Y T E A I K V L P I N A I Y TPR2 (105-138)
PP5 L K T Q A N D Y F K A K D Y E N A I K F Y S Q A I E L N P S N A I Y TPR1 (25-58)
CYP-40 L K N I G N T F F K S Q N W E M A I K K Y A E V L R Y V D S S K A V TPR1 (226-259)

UBP F C N R A A A Y S K L G N Y A G A V Q D C E R A I C I D P A Y S K A TPR3 (128-161)
C. eleg. F C N R A A A Y C R L E Q Y D L A I Q D C R T A L A L D P S Y S K A TPR3 (141-174)
S. cerev. Y A N R A A A H S S L K E Y D Q A V K D A E S A I S I D P S Y F R G TPR3 (139-172)
PP5 Y G N R S L A Y L R T E C Y G Y A L G D A T R A I E L D K K Y I K G TPR2 (59-92)
CYP-40 V L N I G A C K L K M S N W Q G A I D S C L E A L E L D P S N T K A TPR2 (276-309)

UBP Y G R M G L A L S S L N K H V E A V A Y Y K K A L E L D P D N E T Y TPR4 (162-195)
C. eleg. W G R M G L A Y S C Q N R Y E H A A E A Y K K A L E L E P N Q E S Y TPR4 (175-208)
S. cerev. Y S R L G F A K Y A Q G K P E E A L E A Y K K V L D I E G D N A T E TPR4 (173-206)
PP5 Y Y R R A A S N M A L G K F R A A L R D Y E T V V K V K P H D K D A TPR3 (93-126)
CYP-40 L Y R R A Q G W Q G L K E Y D Q A L A D L K K A Q G I A P E D K A I TPR3 (310-343)

FIG. 5A

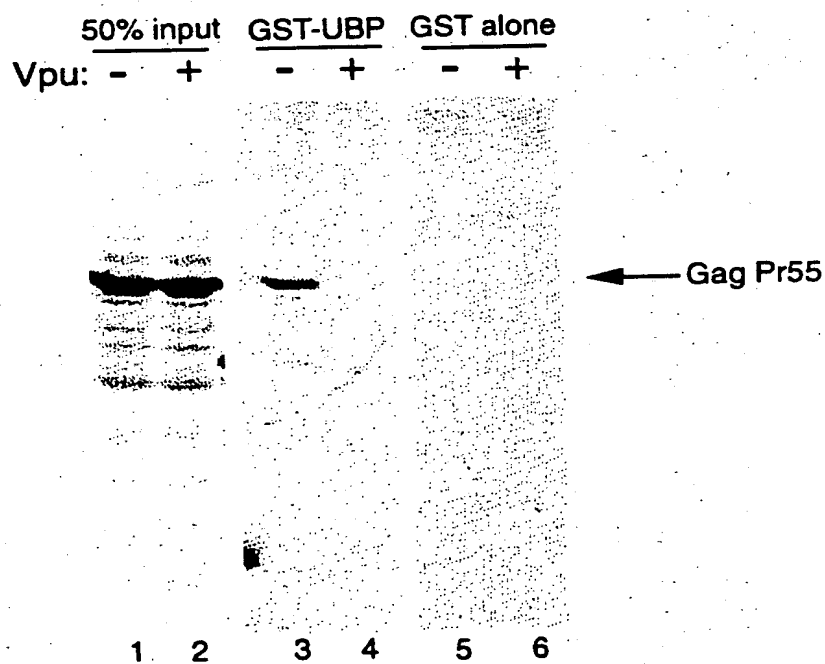
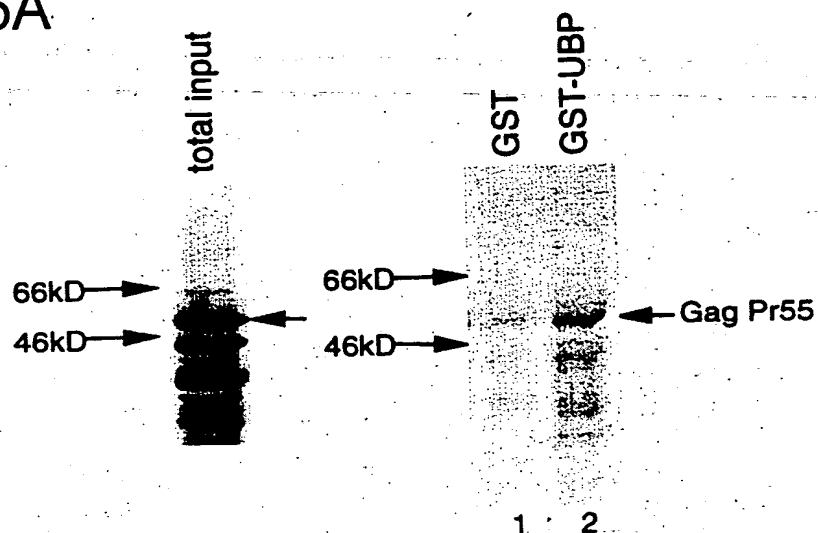


FIG. 5B

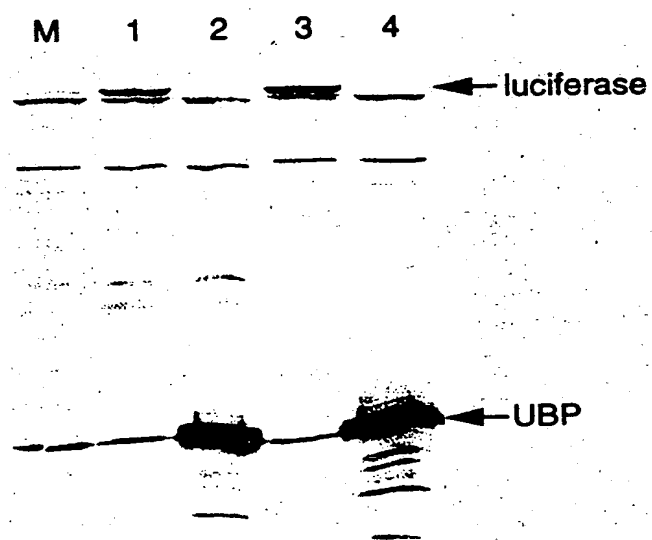


FIG. 6A